SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Genentech, Inc.
                De Sauvage, Frederic J.
                Levin, Nancy
                Vandlen, Richard L.

   (ii) TITLE OF INVENTION: OB Protein Derivatives

  (iii) NUMBER OF SEQUENCES: 2

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Genentech, Inc.
       (B) STREET: 460 Point San Bruno Blvd
       (C) CITY: South San Francisco
       (D) STATE: California
       (E) COUNTRY: USA
       (F) ZIP: 94080

    (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: WinPatin (Genentech)

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE: 19-Dec-1996
       (C) CLASSIFICATION:

  (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 08/667184
       (B) FILING DATE: 20-JUN-1996

  (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 08/579494
       (B) FILING DATE: 27-DEC-1995

 (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Dreger, Ginger R.
       (B) REGISTRATION NUMBER: 33,055
       (C) REFERENCE/DOCKET NUMBER: 985P2PCT

   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: 415/225-3216
       (B) TELEFAX: 415/952-9881
       (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 7127 base pairs
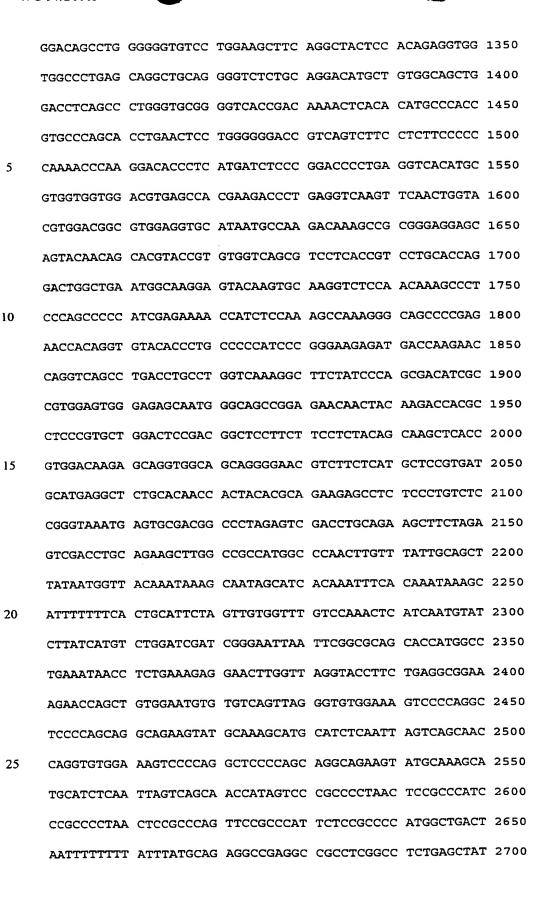   (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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     ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA 200

     TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCAC TTGGCAGTAC 250

     ATCAAGTGTA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT 300

     AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC 350

 10  TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC 400

     GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 450

     TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA 500

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     AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT 600

 15  TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT 650

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     CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA 850

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 25  GAGGCTAACT GAAACACGGA AGGAGACAAT ACCGGAAGGA ACCCGCGCTA 3950

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(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 397 amino acids
          (B) TYPE: Amino Acid
10   (D) TOPOLOGY: Linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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      Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
15   20   25   30

      Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
                          35   40   45

      Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu
                          50   55   60

20   Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met
                          65   70   75

      Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro
                          80   85   90

      Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg
25   95   100   105

      Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro
                          110   115   120

      Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu
                          125   130   135

30   Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
                          140   145   150

      Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
                          155   160   165

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35   170   175   180

      Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

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                        185                    190                    195
        Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                        200                    205                    210

        Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    5                   215                    220                    225

        Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                        230                    235                    240

        Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                        245                    250                    255

   10   Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                        260                    265                    270

        Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                        275                    280                    285

        Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
   15                   290                    295                    300

        Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
                        305                    310                    315

        Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                        320                    325                    330

   20   Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                        335                    340                    345

        Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                        350                    355                    360

        Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
   25                   365                    370                    375

        Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                        380                    385                    390

        Leu Ser Leu Ser Pro Gly Lys
                        395     397
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